explanation of the relevance of EP 0 088 046 and EP 0 133 988 (references BF and BG in the originally filed PTO-1449), as it is presently understood by the individual designated in 37 C.F.R. § 1.56(c) most knowledgeable about the content of each patent. In addition, the substitute PTO-1449 has been amended to remove reference to EP 0 143 949 (reference BH in the originally filed PTO-1449), since this reference was cited twice (*see* reference BC). Finally, the substitute PTO-1449 was amended to remove reference to *Current Protocols In Molecular Biology* (Ausubel *et al.*, eds., John Wiley & Sons 1994); *Remington's Pharmaceutical Sciences* (Gennaro, ed., Mack Publishing 18th ed. 1990); *Computer Analysis of Sequence Data*, Part 1 (Griffin *et al.*, eds., Humana Press 1994); *Sequence Analysis Primer* (Gribskov *et al.*, eds., Oxford University Press 1991); von Heinje, *Sequence Analysis in Molecular Biology* (Academic Press 1987); *Computational Molecular Biology* (Lesk, ed., Oxford University Press 1998); Sambrook, *Molecular Cloning: A Laboratory Manual* (Cold Springs Harbor University Press 1989), *Biocomputing: Informatics and Genome Projects* (Smith, ed., Academic Press 1993); and Steward *et al.*, *Solid Phase Peptide Synthesis* (W.H. Freeman & Co. 1984) (references CC, DL, DM, DO, DP, EA, EL, EN, and EO, respectively, in the originally filed PTO-1449). As these references merely reflect the general state of the art at the time the invention was made, Applicants are unable to specifically indicate or provide copies of the relevant pages.

2. Objection to claims 1-8, 10, 11, 46-48, and 55

The Office Action contains an objection to claims 1-8, 10, 11, 46-48, and 55 as being improperly dependent because the claims are dependent upon a non-elected invention. Applicants have amended claims 1-3 to recite only the elected invention.

3. Objection to specification

The Office Action contains an objection to the specification for containing a space on page 106 between the terms "intracerebral" and "(intra-parenchymal)." Applicants note that there is only a single space between these terms, and that the seemingly irregular spacing is due to the length of the term (*i.e.*, "intracerebroventricular") that immediately follows the term "(intra-parenchymal)."

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4. Rejections of claims 1-8, 10, 11, 46-48, and 55 under 35 U.S.C. § 112, first paragraph

The Office Action asserts a rejection of claims 1-8, 10, 11, 46-48, and 55 under 35 U.S.C. § 112, first paragraph, because the specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to use the invention commensurate in scope with the claims. The Examiner takes the position that the as-filed specification contemplates several methods of gene therapy using the polynucleotides of the claimed invention, and that it would require undue experimentation to determine how to use these polynucleotides in any method of gene therapy.

First, Applicants disagree with the Examiner's assertion that "the elected invention lies in the field of gene therapy" (p. 4 of Office Action). Applicants contend that the pending claims are directed instead to B7-like nucleic acid molecules. Applicants further contend that the B7-like nucleic acid molecules of the claimed invention are enabled for use in, for example, drug candidate screening assays. Specifically, the instant specification provides the nucleotide sequences of a number of B7-like nucleic acid molecules (*e.g.*, SEQ ID NO: 2, SEQ ID NO: 4, and SEQ ID NO: 6), methods for making a transgenic mouse using the claimed B7-like nucleic acid molecules (section entitled "Genetically Engineered Non-Human Animals" beginning at page 74), and guidance for using the transgenic animals of the present invention to screen for drug candidates (p. 75, ln. 7-28). In view of this disclosure, Applicants contend that the instant specification is enabling for use of the invention commensurate in scope with the claims (*i.e.*, B7-like nucleic acid molecules).

In order to provide a reply to the instant Office Action that is fully responsive, Applicants now turn to the particular rejections asserted in the Office Action. The Examiner first asserts that the specification does not enable claims directed to a method of modulating levels of a polypeptide in an animal comprising administering to the animal the nucleic acid molecule of any of Claims 1, 2, or 3, because the claimed invention does not specify the polypeptide in the animal to be modulated. Applicants have amended Claim 55 to indicate that the polypeptide to be modulated is a "B7-like polypeptide." The specification defines the term B7-like polypeptide at page 16, line 23 to page 17, line 3. Applicants respectfully contend that this ground of rejection has been overcome by amendment.

The Examiner next asserts that the specification does not enable claims to a pharmaceutical

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composition comprising a nucleic acid molecule of Claims 1, 2, or 3. In order to expedite prosecution of the instant application, Applicants have canceled claims 46 and 47 without prejudice or disclaimer, rendering this ground of rejection moot. This amendment has been made solely to expedite prosecution and was not made to overcome prior art.

The Examiner also takes the position that it would require undue experimentation to determine the genetic sequences embraced by the claims of the instant application. The Examiner first asserts that it would not be apparent to one of ordinary skill in the art that nucleic acid molecules encoding a polypeptide having a substitution and/or deletion of 1 to 100 amino acid residues in the polypeptide set forth in SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6 would have B7-like polypeptide activity. Applicants have deleted Claim 2(g) of the as-filed specification, rendering this ground of rejection moot. The Examiner next asserts that it would not be apparent to one of ordinary skill in the art how nucleotide sequences complementary to the nucleotide sequences of SEQ ID NO: 1, SEQ ID NO: 3, or SEQ ID NO: 5 would exhibit B7-like polypeptide activity. Applicants contend that Claims 1(e), 2(k), and 3(l) of the as-filed specification are directed to nucleotide sequences that hybridize to nucleotide sequences that are complementary to the nucleotide sequences of the present invention, and are *not themselves* complementary to the nucleotide sequences of the present invention. Applicants therefore assert that it would be apparent to one with skill in the art how the nucleotide sequences of Claims 1(e), 2(k), and 3(l) would exhibit B7-like polypeptide activity, and respectfully request that this ground of rejection be withdrawn.

Applicants respectfully contend that rejections based on 35 U.S.C. § 112, first paragraph, have been overcome by amendment, traversed by argument, or mooted by cancellation of the rejected claims, and request that the Examiner withdraw all rejections made on this basis.

5. Rejections of claims 1-3, 8, 10, and 47 under 35 U.S.C. § 112, second paragraph

The Office Action asserts a rejection of claims 1-3, 8, 10, and 47 under 35 U.S.C. § 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which Applicants regard as the invention. The Examiner takes the position that claims 1-3 are indefinite because the phrase "moderately or highly stringent conditions" is not defined by the claims and the specification does not provide a standard for ascertaining the

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parameters of such conditions. Applicants note that definitions of "moderately stringent conditions" and "highly stringent conditions" are provided in the specification at page 29, lines 4-13 and page 27, lines 13-24, respectively. As an Applicant is entitled to be his or her own lexicographer, these definitions control the interpretation of the phrase "moderately or highly stringent conditions" as it is used in the claims of the instant application, provided that these definitions are not contrary to the meanings of these terms in the art. Moreover, Applicants contend that it would be apparent to one of ordinary skill in the art, in view of the teachings in the instant specification, whether a particular set of hybridization conditions was either "moderately stringent" or "highly stringent." Therefore, Applicants contend that the claims are not indefinite for reciting the phrase "moderately stringent conditions," and respectfully request withdrawal of this ground of rejection.

The Examiner also takes the position that claims 8 and 10 are indefinite because the phrase "B7-like polypeptide" is not defined by the claims and the specification does not provide a standard for ascertaining the meaning of this phrase. Applicants note that an explicit definition of "B7-like polypeptide" is provided in the specification at page 16, line 23 to page 17, line 3, and contend that this definition controls the interpretation of the phrase "B7-like polypeptide" as it is used in the claims of the instant application. Applicants contend, for example, that it would be apparent to one of ordinary skill in the art that a polypeptide comprising the amino acid sequence of SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6 is a B7-like polypeptide. Applicants further contend that it would be apparent to one of ordinary skill in the art that a polypeptide variant (*e.g.*, a polypeptide having at least one conservative amino acid substitution) of the amino acid sequence of SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6 is a B7-like polypeptide, provided that the polypeptide variant has an activity of the polypeptide as set forth in SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6. Therefore, Applicants contend that the claims are not indefinite for reciting the phrase "B7-like polypeptide," and respectfully request withdrawal of this ground of rejection.

The Examiner further takes the position that claim 47 is indefinite because the limitation "[a] composition of claim 46" lacks an antecedent basis. Applicants have canceled claim 47, rendering this ground of rejection moot.

Applicants respectfully contend that rejections based on 35 U.S.C. § 112, second paragraph, have been traversed by argument or mooted by cancellation of the rejected claims, and request that

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the Examiner withdraw all rejections made on this basis.

8. Rejections of claims 1-3 under 35 U.S.C. § 102

The Office Action asserts a rejection of claims 1-3 under 35 U.S.C. § 102, as being anticipated by Marra *et al.* (The Washington University-NCI Mouse EST project, seq_name: gb_est82:BF040046, July 2, 1999; GenBank Accession No. AI790785), contending that Marra *et al.* disclose an EST sequence that shares 85% similarity with the nucleotide sequences set forth in SEQ ID NO: 1, SEQ ID NO: 3, and SEQ ID NO: 5, and therefore would hybridize under moderately stringent conditions to nucleic acid molecules comprising these nucleotide sequences. Applicants traverse this rejection.

Marra *et al.* disclose a nucleotide sequence of 530 bp. SEQ ID NO: 1, SEQ ID NO: 3, and SEQ ID NO: 5 set forth nucleotide sequences of 1146 bp, 1158 bp, and 1158 bp, respectively. Exhibits A-C indicate that there is an overlap of no more than 274 bp or 286 bp between the nucleotide sequence disclosed by Marra *et al.* and the nucleotide sequences set forth in SEQ ID NO: 1, SEQ ID NO: 3, and SEQ ID NO: 5. Exhibits A-C also indicate that in the overlapping regions, the sequences share an identity of between 69.6% to 72.6%, and *not* 85% (Applicants understand the Office Action to mean 85% *identity*, rather than *similarity*, since the term "similarity" refers to the degree of sequence relatedness between two polypeptide sequences, and is defined as such in the instant specification at page 21, lines 6-20). Applicants contend that because the nucleotide sequence of Marra *et al.* and the nucleotide sequences set forth in SEQ ID NO: 1, SEQ ID NO: 3, and SEQ ID NO: 5 share no more than 72.6% identity over no more than 286 bp, a nucleic acid molecule comprising the nucleotide sequence of Marra *et al.* would *not* hybridize under moderately stringent conditions to nucleic acid molecules comprising the nucleotide sequences set forth in SEQ ID NO: 1, SEQ ID NO: 3, or SEQ ID NO: 5. Therefore, Applicants contend that Marra *et al.* does not anticipate claims 1-3, and respectfully request that the Examiner withdraw this rejection.

CONCLUSIONS

Applicants respectfully contend that all conditions of patentability are met in the pending claims as amended. Allowance of the claims is thereby respectfully solicited.

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AMENDMENTS TO THE CLAIMS

Marked Up Versions of Amended Claims under 37 C.F.R. 1.121(c)(1)(ii)

1. (Amended) An isolated nucleic acid molecule comprising ~~a nucleotide sequence selected from~~:

(a) the nucleotide sequence as set forth in any of SEQ ID NOs: 1, SEQ ID NO: 3, or SEQ ID NO: 5 ~~or 7~~;

~~(b) the nucleotide sequence as set forth in SEQ ID NOs: 9, 11 or 13;~~

~~(c)~~(b) a nucleotide sequence encoding the polypeptide as set forth in any of SEQ ID NOs: 2, SEQ ID NO: 4, or SEQ ID NO: 6 ~~or 8~~;

~~(d) a nucleotide sequence encoding the polypeptide as set forth in SEQ ID NOs: 10, 12 or 14;~~

~~(e)~~(c) a nucleotide sequence which hybridizes under at least moderately ~~or highly~~ stringent conditions to the complement of the nucleotide sequence of either (a) or (b), wherein the encoded polypeptide has an activity of the ~~mature form of a~~ polypeptide as set forth in any of SEQ ID NOs: 2, SEQ ID NO: 4, or SEQ ID NO: 6 ~~or 8~~; or

~~(f) a nucleotide sequence which hybridizes under moderately or highly stringent conditions to the complement of (a) or (b), wherein the encoded polypeptide has an activity of the mature form of a polypeptide as set forth in SEQ ID NOs: 10, 12 or 14; and~~

~~(g)~~(d) a nucleotide sequence complementary to the nucleotide sequence of any of (a) - ~~(f)~~(c).

2. (Amended) An isolated nucleic acid molecule comprising ~~a nucleotide sequence selected from~~:

(a) a nucleotide sequence encoding a polypeptide that is at least about 70~~, 75, 80, 85, 90, 95, 96, 97, 98 or 99~~ percent identical to the polypeptide as set forth in any of SEQ ID NOs: 2, SEQ ID NO: 4, or SEQ ID NO: 6 ~~or 8~~, wherein the encoded polypeptide has an activity of the ~~mature form of a~~ polypeptide as set forth in any of SEQ ID NOs: 2, SEQ ID NO: 4, or SEQ ID NO: 6 ~~or 8~~;

~~(b) a nucleotide sequence encoding a polypeptide that is at least about 70, 75, 80, 85, 90, 95, 96, 97, 98 or 99 percent identical to the polypeptide as set forth in SEQ ID NOs: 10, 12 or 14,~~

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~~wherein the polypeptide has an activity of the mature form of a polypeptide as set forth in SEQ ID NOs: 10, 12 or 14;~~

~~(c)~~(b) a nucleotide sequence encoding an allelic variant or splice variant of the nucleotide sequence as set forth in any of SEQ ID NOs: 1, SEQ ID NO: 3, or SEQ ID NO: 5 ~~or 7~~, or the nucleotide sequence of (a), wherein the encoded polypeptide has an activity of the ~~mature form of a~~ polypeptide as set forth in any of SEQ ID NOs: 2, SEQ ID NO: 4, or SEQ ID NO: 6 ~~or 8~~;

~~(d) a nucleotide sequence encoding an allelic variant or splice variant of the nucleotide sequence as set forth in SEQ ID NOs: 9, 11 or 13, wherein the encoded polypeptide has an activity of the mature form of a polypeptide as set forth in SEQ ID NOs: 10, 12 or 14;~~

~~(e)~~(c) a region of the nucleotide sequence of any of SEQ ID NOs: 1, SEQ ID NO: 3, or SEQ ID NO: 5 ~~or 7~~, or the nucleotide sequence of (a) or (b), ~~above,~~ encoding a polypeptide fragment of at least about 25 amino acid residues, wherein the polypeptide fragment has an activity of the ~~mature form of a~~encoded polypeptide as set forth in any of SEQ ID NOs: 2, SEQ ID NO: 4, or SEQ ID NO: 6 ~~or 8~~, or is antigenic;

~~(f) a nucleotide sequence of SEQ ID NOs: 9, 11 or 13, or (a) or (b), above, encoding a polypeptide fragment of at least about 25 amino acid residues, wherein the polypeptide has an activity of the mature form of a polypeptide as set forth in SEQ ID NOs: 10, 12 or 14;~~

~~g) a nucleotide sequence encoding a polypeptide that has a substitution and/or deletion of 1 to 100 amino acid residues as set forth in any of SEQ ID NOs: 1, 3, 5 or 7, wherein the encoded polypeptide has an activity of the mature form of a polypeptide as set forth in SEQ ID NOs: 2, 4, 6 or 8;~~

~~h) a nucleotide sequence encoding a polypeptide that has a substitution and/or deletion of 1 to 100 amino acid residues as set forth in any of SEQ ID NOs: 9, 11 or 13, wherein the encoded polypeptide has an activity of the mature form of a polypeptide as set forth in SEQ ID NOs: 10, 12 or 14;~~

~~(i)~~(d) a region of the nucleotide sequence of any of SEQ ID NOs: 1, SEQ ID NO: 3, or SEQ ID NO: 5 ~~or 7~~, or the nucleotide sequence of any of (a)~~,~~ - (c)~~, (e) or (g), above,~~ comprising a fragment of at least about 16 nucleotides;

~~(j) a nucleotide sequence of SEQ ID NOs: 9, 11 or 13, or (b), (d), (f) or (h), above,~~

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~~comprising a fragment of at least about 16 nucleotides;~~

~~(k)~~(e) a nucleotide sequence which hybridizes under at least moderately ~~or highly~~ stringent conditions to the complement of the nucleotide sequence of any of (a)~~, (c), (e), (g) or (i)~~ - (d)~~, above,~~, wherein the encoded polypeptide has an activity of the ~~mature form of a~~ polypeptide as set forth in any of SEQ ID NOs: 2, SEQ ID NO: 4, or SEQ ID NO: 6 ~~or 8~~; or

~~(l) a nucleotide sequence which hybridizes under moderately or highly stringent conditions to the complement of any of (b), (d), (f), (h) or (j), above, wherein the polypeptide has an activity of the mature form of a polypeptide as set forth in SEQ ID NOs: 10, 12 or 14; and~~

~~(m)~~(f) a nucleotide sequence complementary to the nucleotide sequence of any of (a) - ~~(l)~~(e).

3. (Amended) An isolated nucleic acid molecule comprising ~~a nucleotide sequence selected from~~:

(a) a nucleotide sequence encoding a polypeptide as set forth in any of SEQ ID NOs: 2, SEQ ID NO: 4, or SEQ ID NO: 6 ~~or 8~~ with at least one conservative amino acid substitution, wherein the encoded polypeptide has an activity of the ~~mature form of a~~ polypeptide as set forth in any of SEQ ID NOs: 2, SEQ ID NO: 4, or SEQ ID NO: 6 ~~or 8~~;

~~(b) a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NOs: 10, 12 or 14 with at least one conservative amino acid substitution, wherein the polypeptide has an activity of the mature form of a polypeptide as set forth in SEQ ID NOs: 10, 12 or 14;~~

~~(c)~~(b) a nucleotide sequence encoding a polypeptide as set forth in any of SEQ ID NOs: 2, SEQ ID NO: 4, or SEQ ID NO: 6 ~~or 8~~ with at least one amino acid insertion, wherein the encoded polypeptide has an activity of the ~~mature form of a~~ polypeptide as set forth in any of SEQ ID NOs: 2, SEQ ID NO: 4, or SEQ ID NO: 6 ~~or 8~~;

~~(d) a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NOs: 10, 12 or 14 with at least one amino acid insertion, wherein the polypeptide has an activity of the mature form of a polypeptide as set forth in SEQ ID NOs: 10, 12 or 14;~~

~~(e)~~(c) a nucleotide sequence encoding a polypeptide as set forth in any of SEQ ID NOs: 2, SEQ ID NO: 4, or SEQ ID NO: 6 ~~or 8~~ with at least one amino acid deletion, wherein the encoded polypeptide has an activity of the ~~mature form of a~~ polypeptide as set forth in any of SEQ ID NOs: 2,

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SEQ ID NO: 4, or SEQ ID NO: 6 ~~or 8~~;

~~(f) a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NOs: 10, 12 or 14 with at least one amino acid deletion, wherein the polypeptide has an activity of the mature form of a polypeptide as set forth in SEQ ID NOs: 10, 12 or 14;~~

~~(g)~~(d) a nucleotide sequence encoding a polypeptide as set forth in any of SEQ ID NOs: 2, SEQ ID NO: 4, or SEQ ID NO: 6 ~~or 8~~ which has a C- and/or N- terminal truncation, wherein the encoded polypeptide has an activity of the ~~mature form of a~~ polypeptide as set forth in any of SEQ ID NOs: 2, SEQ ID NO: 4, or SEQ ID NO: 6 ~~or 8~~;

~~(h) a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NOs: 10, 12 or 14 which has a C- and/or N- terminal truncation, wherein the polypeptide has an activity of the mature form of a polypeptide as set forth in SEQ ID NOs: 10, 12 or 14;~~

~~(i)~~(e) a nucleotide sequence encoding a polypeptide as set forth in any of SEQ ID NOs: 2, SEQ ID NO: 4, or SEQ ID NO: 6 ~~or 8~~ with at least one modification that is a ~~selected from at least one~~ conservative amino acid substitution, an amino acid insertion, an amino acid deletion, C-terminal truncation, ~~and~~or N-terminal truncation, wherein the encoded polypeptide has an activity of the ~~mature form of a~~ polypeptide as set forth in any of SEQ ID NOs: 2, SEQ ID NO: 4, or SEQ ID NO: 6 ~~or 8~~;

~~(j) a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NOs: 10, 12 or 14 with at least one modification selected from at least one amino acid substitution, amino acid insertion, amino acid deletion, C-terminal truncation, and N-terminal truncation, wherein the polypeptide has an activity of the mature form of a polypeptide as set forth in SEQ ID NOs: 10, 12 or 14;~~

~~(k)~~(f) a nucleotide sequence of any of (a) - ~~(j)~~(e) comprising a fragment of at least about 16 nucleotides;

~~(l)~~(g) a nucleotide sequence which hybridizes under at least moderately ~~or highly~~ stringent conditions to the complement of the nucleotide sequence of any of (a) ~~, (c), (e), (g), (i) or (k)~~ - (f) ~~,~~, wherein the encoded polypeptide has an activity of the ~~mature form of a~~ polypeptide as set forth in any of SEQ ID NOs: 2, SEQ ID NO: 4, or SEQ ID NO: 6 ~~or 8~~; or

~~(m) a nucleotide sequence which hybridizes under moderately or highly stringent~~

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~~conditions to the complement of any of (b), (d), (f), (h), (j) or (k), wherein the polypeptide has an activity of the mature form of a polypeptide as set forth in SEQ ID NOs: 10, 12 or 14;and~~

~~(n)~~(h) a nucleotide sequence complementary to the nucleotide sequence of any of (a) - ~~(m)~~(g).

4. (Amended) A vector comprising the nucleic acid molecule of any of Claims 1, 2, or 3.

11. (Amended) The isolated nucleic acid molecule according to Claim 2, wherein the percent identity is determined using a computer program ~~selected from~~ that is GAP, ~~BLASTP,~~ BLASTN, FASTA, BLASTA, BLASTX, BestFit, ~~and~~or the Smith-Waterman algorithm.

48. (Amended) A viral vector comprising a nucleic acid molecule of any of Claims 1, 2, or 3.

55. (Amended) A method of modulating levels of a B7-like polypeptide in an animal comprising administering to the animal the nucleic acid molecule of any of Claims 1, 2, or 3.

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EXHIBIT A

```
                  10          20          30          40          50          60
                   *   *       *   *       *   *       *   *       *   *       *   *
SEQ01_ORF     ATGGGGCTTG TGATTTTCCT CCACGGTTCT GGGTCTGGTA ATGAAGTCAT AGAAGGCCCC
              TACCCCGAAC ACTAAAAGGA GGTGCCAAGA CCCAGACCAT TACTTCAGTA TCTTCCGGGG
                        |           |           |           |           |           |
                 260    |   270     |   280     |   290     |   300     |   310     |
Marra EST     cTGGtcaTcc TGgcTcagCT gacaGcTTCc GGaTCcaGTt ATcAgaTCAT AGAAGGtCCt>
               |||   |   ||  |  ||     | |||  || ||  ||  || |  |||| ||||||  ||
SEQ01_ORF     ATGGGGCTTG TGATTTTCCT CCACGGTTCT GGGTCTGGTA ATGAAGTCAT AGAAGGCCCC

                  70          80          90          100         110         120
                   *   *       *   *       *   *       *   *       *   *       *   *
SEQ01_ORF     CAGAATGCAA CAGTCCTGAA GGGCTCCCAG GCTCGCTTCA ACTGCACCGT CTCCCAGGGC
              GTCTTACGTT GTCAGGACTT CCCGAGGGTC CGAGCGAAGT TGACGTGGCA GAGGGTCCCG
                        |           |           |           |           |           |
                 320    |   330     |   340     |   350     |   360     |   370     |
Marra EST     CAGAATGtAA CAGTCCTaAA GGaCTCagAG GCTCaCTTCA ACTGCACCGT gaCtCAcGGC>
              |||||||  ||  |||||||  ||  ||  |||  ||  ||||  |||||  ||||||||||    |  ||  |||
SEQ01_ORF     CAGAATGCAA CAGTCCTGAA GGGCTCCCAG GCTCGCTTCA ACTGCACCGT CTCCCAGGGC

                 130         140         150         160         170         180
                  *   *       *   *       *   *       *   *       *   *       *   *
SEQ01_ORF     TGGAAGCTCA TCATGTGGGC TCTCAGTGAC ATGGTGGTGC TAAGCGTCAG GCCCATGGAG
              ACCTTCGAGT AGTACACCCG AGAGTCACTG TACCACCACG ATTCGCAGTC CGGGTACCTC
                        |           |           |           |           |           |
                        |           |           |           |        a  |           |
                        |           |           |           |        |  |           |
                 380    |   390     |   400     |   410     |   420  |  |  430      |
Marra EST     TGGAAGCTtc TCATGTGGaC TCTtAaccAa ATGGTGGTGC TgAGtcTCcc aCCCAaGG-a>
              ||||||||   ||||||||  |  |||  |   |  ||||||||||  |  ||   ||    ||||  ||
SEQ01_ORF     TGGAAGCTCA TCATGTGGGC TCTCAGTGAC ATGGTGGTGC TAAGCGTCAG GCCCATGGAG

                 190         200         210         220         230         240
                  *   *       *   *       *   *       *   *       *   *       *   *
SEQ01_ORF     CCCATCATCA CCAATGACCG CTTCACCTCT CAGAGGTACG ACCAGGGCGG GAACTTCACC
              GGGTAGTAGT GGTTACTGGC GAAGTGGAGA GTCTCCATGC TGGTCCCGCC CTTGAAGTGG
                        |           |           |           |           |           |
                        |           |           |           |        c  |           |
                        |           |           |           |        |  |           |
                 440    |   450     |   460     |   470     |   480  |  |  490      |
Marra EST     CCCATCATCA CCAAcaACCG tTTCACCTaT gccAGtTA-c AaCAGcatGa cAgCTTCAtC>
              ||||||||||  ||||  ||||  |||||||  |    ||  ||   |  |||   |   |  |||||  |
SEQ01_ORF     CCCATCATCA CCAATGACCG CTTCACCTCT CAGAGGTACG ACCAGGGCGG GAACTTCACC

                 250         260         270         280         290         300
                  *   *       *   *       *   *       *   *       *   *       *   *
SEQ01_ORF     TCGGAGATGA TCATCCACAA TGTGGAGCCC AGTGATTCGG GGAACATCAG ATGCAGCCTC
              AGCCTCTACT AGTAGGTGTT ACACCTCGGG TCACTAAGCC CCTTGTAGTC TACGTCGGAG
                        |           |           |           |           |           |
                 500    |   510     |   520     |           |           |           |
Marra EST     TCGGAGtTGA TCATCCAtgA TGTGcAGCCC AGTG>       |           |           |
              ||||||  |||  |||||||  |  ||||  |||||  ||||    |           |           |
SEQ01_ORF     TCGGAGATGA TCATCCACAA TGTGGAGCCC AGTG        |           |           |
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                 310         320         330         340         350         360
                  *   *       *   *       *   *       *   *       *   *       *   *
SEQ01_ORF   CAGAACAGTC GCCTGCATGG ATCTGCTTAC CTTACCGTCC AAGTTATGGG AGAGCTGTTC
            GTCTTGTCAG CGGACGTACC TAGACGAATG GAATGGCAGG TTCAATACCC TCTCGACAAG

                 370         380         390         400         410         420
                  *   *       *   *       *   *       *   *       *   *       *   *
SEQ01_ORF   ATTCCCAGTG TTAATCTTGT AGTCGCTGAG AATGAACCTT GTGAAGTTAC TTGTCTACCC
            TAAGGGTCAC AATTAGAACA TCAGCGACTC TTACTTGGAA CACTTCAATG AACAGATGGG

                 430         440         450         460         470         480
                  *   *       *   *       *   *       *   *       *   *       *   *
SEQ01_ORF   TCACACTGGA CCCGGCTCCC GGATATTTCC TGGGAGCTCG GTCTCCTGGT CAGCCATTCA
            AGTGTGACCT GGGCCGAGGG CCTATAAAGG ACCCTCGAGC CAGAGGACCA GTCGGTAAGT

                 490         500         510         520         530         540
                  *   *       *   *       *   *       *   *       *   *       *   *
SEQ01_ORF   AGCTATTATT TTGTTCCGGA GCCCAGCGAC CTTCAAAGTG CAGTGAGCAT CCTGGCTCTG
            TCGATAATAA AACAAGGCCT CGGGTCGCTG GAAGTTTCAC GTCACTCGTA GGACCGAGAC

                 550         560         570         580         590         600
                  *   *       *   *       *   *       *   *       *   *       *   *
SEQ01_ORF   ACCCCACAGA GCAATGGGAC TTTGACTTGC GTGGCTACCT GGAAGAGCCT GAAGGCCCGC
            TGGGGTGTCT CGTTACCCTG AAACTGAACG CACCGATGGA CCTTCTCGGA CTTCCGGGCG

                 610         620         630         640         650         660
                  *   *       *   *       *   *       *   *       *   *       *   *
SEQ01_ORF   AAGTCTGCAA CTGTAAATCT CACTGTGATT CGGTGTCCCC AAGACACTGG AGGTGGTATT
            TTCAGACGTT GACATTTAGA GTGACACTAA GCCACAGGGG TTCTGTGACC TCCACCATAA

                 670         680         690         700         710         720
                  *   *       *   *       *   *       *   *       *   *       *   *
SEQ01_ORF   AATATTCCAG GTGTATTATC AAGTTTACCG AGTTTAGGTT TTTCATTGCC TACTTGGGGC
            TTATAAGGTC CACATAATAG TTCAAATGGC TCAAATCCAA AAAGTAACGG ATGAACCCCG

                 730         740         750         760         770         780
                  *   *       *   *       *   *       *   *       *   *       *   *
SEQ01_ORF   AAAGTTGGAC TTGGACTAGC AGGCACCATG CTTCTGACGC CGACGTGTAC TCTTACAATA
            TTTCAACCTG AACCTGATCG TCCGTGGTAC GAAGACTGCG GCTGCACATG AGAATGTTAT

                 790         800         810         820         830         840
                  *   *       *   *       *   *       *   *       *   *       *   *
SEQ01_ORF   CGCTGCTGCT GCTGCCGCCG TCGTTGTTGT GGCTGCAACT GCTGCTGCCG TTGTTGTTTC
            GCGACGACGA CGACGGCGGC AGCAACAACA CCGACGTTGA CGACGACGGC AACAACAAAG

                 850         860         870         880         890         900
                  *   *       *   *       *   *       *   *       *   *       *   *
SEQ01_ORF   TGCTGTAGAA GAAAAAGAGG ATTTCGTATT CAATTTCAAA AGAAATCTGA AAAAGAGAAG
            ACGACATCTT CTTTTTCTCC TAAAGCATAA GTTAAAGTTT TCTTTAGACT TTTTCTCTTC
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                  910         920         930         940         950         960
                   *   *       *   *       *   *       *   *       *   *       *   *
SEQ01_ORF     ACAAACAAAG AAACTGAGAC AGAAAGTGGA AATGAAAACT CCGGCTACAA TTCAGATGAA
              TGTTTGTTTC TTTGACTCTG TCTTTCACCT TTACTTTTGA GGCCGATGTT AAGTCTACTT

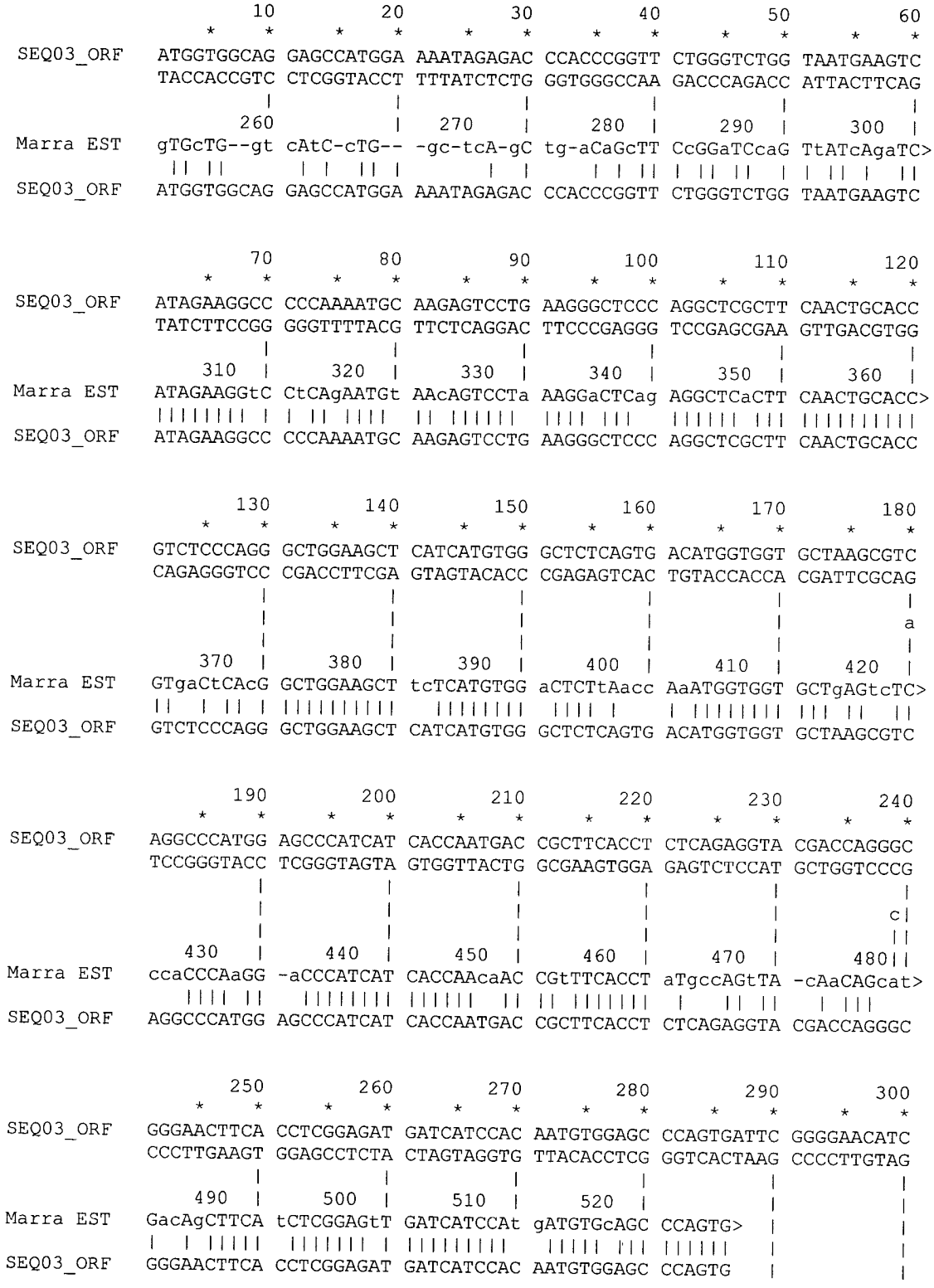
                  970         980         990        1000        1010        1020
                   *   *       *   *       *   *       *   *       *   *       *   *
SEQ01_ORF     CAAAAGACCA CAGACACCGC TTCTCTCCCT CCCAAATCCT GTGAATCCAG TGATCCTGAA
              GTTTTCTGGT GTCTGTGGCG AAGAGAGGGA GGGTTTAGGA CACTTAGGTC ACTAGGACTT

                 1030        1040        1050        1060        1070        1080
                   *   *       *   *       *   *       *   *       *   *       *   *
SEQ01_ORF     CAAAGAAACA GTAGCTGTGG CCCTCCTCAC CAGCGGGCTG ATCAACGTCC ACCCAGGCCA
              GTTTCTTTGT CATCGACACC GGGAGGAGTG GTCGCCCGAC TAGTTGCAGG TGGGTCCGGT

                 1090        1100        1110        1120        1130        1140
                   *   *       *   *       *   *       *   *       *   *       *   *
SEQ01_ORF     GCAAGTCATC CACAGGCTTC TTTTAATCTG GCCAGTCCTG AGAAGGTCAG TAATACAACT
              CGTTCAGTAG GTGTCCGAAG AAAATTAGAC CGGTCAGGAC TCTTCCAGTC ATTATGTTGA

                   *
SEQ01_ORF     GTAGTA
              CATCAT
```

EXHIBIT B



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                  310         320         330         340         350         360
                  *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
SEQ03_ORF         AGATGCAGCC TCCAGAACAG TCGCCTGCAT GGATCTGCTT ACCTTACCGT CCAAGTTATG
                  TCTACGTCGG AGGTCTTGTC AGCGGACGTA CCTAGACGAA TGGAATGGCA GGTTCAATAC

                  370         380         390         400         410         420
                  *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
SEQ03_ORF         GGAGAGCTGT TCATTCCCAG TGTTAATCTT GTAGTCGCTG AGAATGAACC TTGTGAAGTT
                  CCTCTCGACA AGTAAGGGTC ACAATTAGAA CATCAGCGAC TCTTACTTGG AACACTTCAA

                  430         440         450         460         470         480
                  *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
SEQ03_ORF         ACTTGTCTAC CCTCACACTG GACCTGGCTC CCGGATATTT CCTGGGAGCT CGGTCTCCTG
                  TGAACAGATG GGAGTGTGAC CTGGACCGAG GGCCTATAAA GGACCCTCGA GCCAGAGGAC

                  490         500         510         520         530         540
                  *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
SEQ03_ORF         GTCAGCCATT CAAGCTATTA TTTTGTTCCG GAGCCCAGCG ACCTTCAAAG TGCAGTGAGC
                  CAGTCGGTAA GTTCGATAAT AAAACAAGGC CTCGGGTCGC TGGAAGTTTC ACGTCACTCG

                  550         560         570         580         590         600
                  *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
SEQ03_ORF         ATCCTGGCTC TGACCCCACA GAGCAATGGG ACTTTGACTT GCGTGGCTAC CTGGAAGAGC
                  TAGGACCGAG ACTGGGGTGT CTCGTTACCC TGAAACTGAA CGCACCGATG GACCTTCTCG

                  610         620         630         640         650         660
                  *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
SEQ03_ORF         CTGAAGGCCC GCAAGTCTGC AACTGTAAAT CTCACTGTGA TTCGGTGTCC CCAAGACACT
                  GACTTCCGGG CGTTCAGACG TTGACATTTA GAGTGACACT AAGCCACAGG GGTTCTGTGA

                  670         680         690         700         710         720
                  *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
SEQ03_ORF         GGAGGTGGTA TTAATATTCC AGGTGTATTA TCAAGTTTAC CGAGTTTAGG TTTTTCATTG
                  CCTCCACCAT AATTATAAGG TCCACATAAT AGTTCAAATG GCTCAAATCC AAAAAGTAAC

                  730         740         750         760         770         780
                  *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
SEQ03_ORF         CCTACTTGGG GCAAAGTTGG ACTTGGACTA GCAGGCACCA TGCTTCTGAC GCCGACGTGT
                  GGATGAACCC CGTTTCAACC TGAACCTGAT CGTCCGTGGT ACGAAGACTG CGGCTGCACA

                  790         800         810         820         830         840
                  *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
SEQ03_ORF         ACTCTTACAA TACGCTGCTG CTGCTGCCGC CGTCGTTGTT GTGGCTGCAA CTGCTGCTGC
                  TGAGAATGTT ATGCGACGAC GACGACGGCG GCAGCAACAA CACCGACGTT GACGACGACG

                  850         860         870         880         890         900
                  *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
SEQ03_ORF         CGTTGTTGTT TCTGCTGTAG AAGAAAAAGA GGATTTCGTA TTCAATTTCA AAAGAAATCT
                  GCAACAACAA AGACGACATC TTCTTTTTCT CCTAAAGCAT AAGTTAAAGT TTTCTTTAGA
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                 910        920        930        940        950        960
                 *    *     *    *     *    *     *    *     *    *     *    *
SEQ03_ORF        GAAAAAGAGA AGACAAACAA AGAAACTGAG ACAGAAAGTG GAAATGAAAA CTCCGGCTAC
                 CTTTTTCTCT TCTGTTTGTT TCTTTGACTC TGTCTTTCAC CTTTACTTTT GAGGCCGATG

                 970        980        990       1000       1010       1020
                 *    *     *    *     *    *     *    *     *    *     *    *
SEQ03_ORF        AATTCAGATG AACAAAAGAC CACAGACACC GCTTCTCTCC CTCCCAAATC CTGTGAATCC
                 TTAAGTCTAC TTGTTTTCTG GTGTCTGTGG CGAAGAGAGG GAGGGTTTAG GACACTTAGG

                1030       1040       1050       1060       1070       1080
                *    *     *    *     *    *     *    *     *    *     *    *
SEQ03_ORF        AGTGATCCTG AACAAAGAAA CAGTAGCTGT GGCCCTCCTC ACCAGCGGGC TGATCAACGT
                 TCACTAGGAC TTGTTTCTTT GTCATCGACA CCGGGAGGAG TGGTCGCCCG ACTAGTTGCA

                1090       1100       1110       1120       1130       1140
                *    *     *    *     *    *     *    *     *    *     *    *
SEQ03_ORF        CCACCCAGGC CAGCAAGTCA TCCACAGGCT TCTTTTAATC TGGCCAGTCC TGAGAAGGTC
                 GGTGGGTCCG GTCGTTCAGT AGGTGTCCGA AGAAAATTAG ACCGGTCAGG ACTCTTCCAG

                1150
                *    *     *
SEQ03_ORF        AGTAATACAA CTGTAGTA
                 TCATTATGTT GACATCAT
```

EXHIBIT C

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                  10         20         30         40         50         60
                   *  *       *  *       *  *       *  *       *  *       *  *
SEQ05_ORF    ATGGAAAGGC ATTTGCTCAC GGTTCCAGAA GCTGTAGGTT CTGGGTCTGG TAATGAAGTC
             TACCTTTCCG TAAACGAGTG CCAAGGTCTT CGACATCCAA GACCCAGACC ATTACTTCAG
                      |          |          |          |          |          |
                 250  |     260  |     270  |     280  |     290  |     300  |
Marra EST    cTGGctgtGC tggTcaTCct GGc-tCAGct --gacAGcTT CcGGaTCcaG TtATcAgaTC>
              |||   ||    |  ||   ||   |||       || ||  | || ||  | | || |  ||
SEQ05_ORF    ATGGAAAGGC ATTTGCTCAC GGTTCCAGAA GCTGTAGGTT CTGGGTCTGG TAATGAAGTC

                  70         80         90        100        110        120
                   *  *       *  *       *  *       *  *       *  *       *  *
SEQ05_ORF    ATAGAAGGCC CCCAGAATGC AACAGTCCTG AAGGGCTCCC AGGCTCGCTT CAACTGCACC
             TATCTTCCGG GGGTCTTACG TTGTCAGGAC TTCCCGAGGG TCCGAGCGAA GTTGACGTGG
                      |          |          |          |          |          |
                 310  |     320  |     330  |     340  |     350  |     360  |
Marra EST    ATAGAAGGtC CtCAGAATGt AACAGTCCTa AAGGaCTCag AGGCTCaCTT CAACTGCACC>
             |||||||| | | |||||||  |||||||||  ||||  |||   ||||||  |||  ||||||||||
SEQ05_ORF    ATAGAAGGCC CCCAGAATGC AACAGTCCTG AAGGGCTCCC AGGCTCGCTT CAACTGCACC

                 130        140        150        160        170        180
                   *  *       *  *       *  *       *  *       *  *       *  *
SEQ05_ORF    GTCTCCCAGG GCTGGAAGCT CATCATGTGG GCTCTCAGTG ACATGGTGGT GCTAAGCGTC
             CAGAGGGTCC CGACCTTCGA GTAGTACACC CGAGAGTCAC TGTACCACCA CGATTCGCAG
                      |          |          |          |          |          |
                      |          |          |          |          |          a
                      |          |          |          |          |          |
                 370  |     380  |     390  |     400  |     410  |     420  |
Marra EST    GTgaCtCAcG GCTGGAAGCT tcTCATGTGG aCTCTtAacc AaATGGTGGT GCTgAGtcTC>
             ||  | || | ||||||||||   ||||||||  ||||  |    | ||||||||  ||| ||  ||
SEQ05_ORF    GTCTCCCAGG GCTGGAAGCT CATCATGTGG GCTCTCAGTG ACATGGTGGT GCTAAGCGTC

                 190        200        210        220        230        240
                   *  *       *  *       *  *       *  *       *  *       *  *
SEQ05_ORF    AGGCCCATGG AGCCCATCAT CACCAATGAC CGCTTCACCT CTCAGAGGTA CGACCAGGGC
             TCCGGGTACC TCGGGTAGTA GTGGTTACTG GCGAAGTGGA GAGTCTCCAT GCTGGTCCCG
                      |          |          |          |          |          |
                      |          |          |          |          |          c|
                      |          |          |          |          |          ||
                 430  |     440  |     450  |     460  |     470  |      480||
Marra EST    ccaCCCAaGG -aCCCATCAT CACCAAcaAC CGtTTCACCT aTgccAGtTA -cAaCAGcat>
               ||||  ||   ||||||||  ||||||  ||  || |||||||  |   ||  ||   | |||
SEQ05_ORF    AGGCCCATGG AGCCCATCAT CACCAATGAC CGCTTCACCT CTCAGAGGTA CGACCAGGGC

                 250        260        270        280        290        300
                   *  *       *  *       *  *       *  *       *  *       *  *
SEQ05_ORF    GGGAACTTCA CCTCGGAGAT GATCATCCAC AATGTGGAGC CCAGTGATTC GGGGAACATC
             CCCTTGAAGT GGAGCCTCTA CTAGTAGGTG TTACACCTCG GGTCACTAAG CCCCTTGTAG
                      |          |          |          |          |          |
                 490  |     500  |     510  |     520  |          |          |
Marra EST    GacAgCTTCA tCTCGGAGtT GATCATCCAt gATGTGcAGC CCAGTG>   |          |
             |  | |||||  |||||||  | |||||||||   |||||  |||  ||||||   |          |
SEQ05_ORF    GGGAACTTCA CCTCGGAGAT GATCATCCAC AATGTGGAGC CCAGTG    |          |
```

```
                 310         320         330         340         350         360
                  *   *       *   *       *   *       *   *       *   *       *   *
SEQ05_ORF    AGATGCAGCC TCCAGAACAG TCGCCTGCAT GGATCTGCTT ACCTTACCGT CCAAGTTATG
             TCTACGTCGG AGGTCTTGTC AGCGGACGTA CCTAGACGAA TGGAATGGCA GGTTCAATAC

                 370         380         390         400         410         420
                  *   *       *   *       *   *       *   *       *   *       *   *
SEQ05_ORF    GGAGAGCTGT TCATTCCCAG TGTTAATCTT GTAGTCGCTG AGAATGAACC TTGTGAAGTT
             CCTCTCGACA AGTAAGGGTC ACAATTAGAA CATCAGCGAC TCTTACTTGG AACACTTCAA

                 430         440         450         460         470         480
                  *   *       *   *       *   *       *   *       *   *       *   *
SEQ05_ORF    ACTTGTCTAC CCTCACACTG GACCCGGCTC CCGGATATTT CCTGGGAGCT CGGTCTCCTG
             TGAACAGATG GGAGTGTGAC CTGGGCCGAG GGCCTATAAA GGACCCTCGA GCCAGAGGAC

                 490         500         510         520         530         540
                  *   *       *   *       *   *       *   *       *   *       *   *
SEQ05_ORF    GTCAGCCATT CAAGCTATTA TTTTGTTCCG GAGCCCAGCG ACCTTCAAAG TGCAGTGAGC
             CAGTCGGTAA GTTCGATAAT AAAACAAGGC CTCGGGTCGC TGGAAGTTTC ACGTCACTCG

                 550         560         570         580         590         600
                  *   *       *   *       *   *       *   *       *   *       *   *
SEQ05_ORF    ATCCTGGCTC TGACCCCACA GAGCAATGGG ACTTTGACTT GCGTGGCTAC CTGGAAGAGC
             TAGGACCGAG ACTGGGGTGT CTCGTTACCC TGAAACTGAA CGCACCGATG GACCTTCTCG

                 610         620         630         640         650         660
                  *   *       *   *       *   *       *   *       *   *       *   *
SEQ05_ORF    CTGAAGGCCC GCAAGTCTGC AACTGTAAAT CTCACTGTGA TTCGGTGTCC CCAAGACACT
             GACTTCCGGG CGTTCAGACG TTGACATTTA GAGTGACACT AAGCCACAGG GGTTCTGTGA

                 670         680         690         700         710         720
                  *   *       *   *       *   *       *   *       *   *       *   *
SEQ05_ORF    GGAGGTGGTA TTAATATTCC AGGTGTATTA TCAAGTTTAC CGAGTTTAGG TTTTTCATTG
             CCTCCACCAT AATTATAAGG TCCACATAAT AGTTCAAATG GCTCAAATCC AAAAAGTAAC

                 730         740         750         760         770         780
                  *   *       *   *       *   *       *   *       *   *       *   *
SEQ05_ORF    CCTACTTGGG GCAAAGTTGG ACTTGGACTA GCAGGCACCA TGCTTCTGAC GCCGACGTGT
             GGATGAACCC CGTTTCAACC TGAACCTGAT CGTCCGTGGT ACGAAGACTG CGGCTGCACA

                 790         800         810         820         830         840
                  *   *       *   *       *   *       *   *       *   *       *   *
SEQ05_ORF    ACTCTTACAA TACGCTGCTG CTGCTGCCGC CGTCGTTGTT GTGGCTGCAA CTGCTGCTGC
             TGAGAATGTT ATGCGACGAC GACGACGGCG GCAGCAACAA CACCGACGTT GACGACGACG

                 850         860         870         880         890         900
                  *   *       *   *       *   *       *   *       *   *       *   *
SEQ05_ORF    CGTTGTTGTT TCTGCTGTAG AAGAAAAAGA GGATTTCGTA TTCAATTTCA AAAGAAATCT
             GCAACAACAA AGACGACATC TTCTTTTTCT CCTAAAGCAT AAGTTAAAGT TTTCTTTAGA
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                 910         920         930         940         950         960
                  *   *       *   *       *   *       *   *       *   *       *   *
SEQ05_ORF   GAAAAAGAGA AGACAAACAA AGAAACTGAG ACAGAAAGTG GAAATGAAAA CTCCGGCTAC
            CTTTTTCTCT TCTGTTTGTT TCTTTGACTC TGTCTTTCAC CTTTACTTTT GAGGCCGATG

                 970         980         990        1000        1010        1020
                  *   *       *   *       *   *       *   *       *   *       *   *
SEQ05_ORF   AATTCAGATG AACAAAAGAC CACAGAAACC GCTTCTCTCC CTCCCAAATC CTGTGAATCC
            TTAAGTCTAC TTGTTTTCTG GTGTCTTTGG CGAAGAGAGG GAGGGTTTAG GACACTTAGG

                1030        1040        1050        1060        1070        1080
                  *   *       *   *       *   *       *   *       *   *       *   *
SEQ05_ORF   AGTGATCCTG AACAAAGAAA CAGTAGCTGT GGCCCTCCTC ACCAGCGGGC TGATCAACGT
            TCACTAGGAC TTGTTTCTTT GTCATCGACA CCGGGAGGAG TGGTCGCCCG ACTAGTTGCA

                1090        1100        1110        1120        1130        1140
                  *   *       *   *       *   *       *   *       *   *       *   *
SEQ05_ORF   CCACCCAGGC CAGCAAGTCA TCCACAGGCT TCTTTTAATC TGGCCAGTCC TGAGAAGGTC
            GGTGGGTCCG GTCGTTCAGT AGGTGTCCGA AGAAAATTAG ACCGGTCAGG ACTCTTCCAG

                1150
                  *   *       *
SEQ05_ORF   AGTAATACAA CTGTAGTA
            TCATTATGTT GACATCAT
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